<110> Wang, Tongwen

<120> Composistions and Methods of modulating TGF-B Signaling

<130> 17633/1082

<140> 09927738
<141> 2001-08-10

<150> US 60/119786
<151> 1999-02-11

<150> PCT/US00/03561
<151> 2000-02-11

<160> 28

<170> PatentIn version 3.1

<210> 1
<211> 277
<212> PRT
<213> Unknown

<220>
<223> Isolated using yeast two hybrid system, Clone S1 + 27
<400> 1

Lys Ser Ser Pro Leu Leu Ile Arg Met Glu Glu Ser Leu Asn Ile Val
1   5   10   15

Lys Tyr Thr Ala Phe Leu Tyr Asn Asp Gln Leu Ile Trp Ser Gly Leu

```
                    20                      25                 30

Glu Gln Asp Asp Met Arg Ile Leu Tyr Lys Tyr Leu Thr Thr Ser Leu
        35              40              45

Phe Pro Arg His Ile Glu Pro Glu Leu Ala Gly Arg Asp Ser Pro Ile
    50              55              60

Arg Ala Glu Met Pro Gly Asn Leu Gln His Tyr Gly Arg Phe Leu Thr
65              70              75                          80

Gly Pro Leu Asn Leu Asn Asp Pro Asp Ala Lys Cys Arg Phe Pro Lys
            85              90                      95

Ile Phe Val Asn Thr Asp Asp Thr Tyr Glu Glu Leu His Leu Ile Val
            100             105             110

Tyr Lys Ala Met Ser Ala Ala Val Cys Phe Met Ile Asp Ala Ser Val
        115             120             125

His Pro Thr Leu Asp Phe Cys Arg Arg Leu Asp Ser Ile Val Gly Pro
    130             135             140

Gln Leu Thr Val Leu Ala Ser Asp Ile Cys Glu Gln Phe Asn Ile Asn
145             150             155             160

Lys Arg Met Ser Gly Ser Glu Lys Glu Pro Gln Phe Lys Phe Ile Tyr
            165             170             175

Phe Asn His Met Asn Leu Ala Glu Lys Ser Thr Val His Met Arg Lys
            180             185             190

Thr Pro Ser Val Ser Leu Thr Ser Val His Pro Asp Leu Met Lys Ile
        195             200             205

Leu Gly Asp Ile Asn Ser Asp Phe Thr Arg Val Asp Glu Asp Glu Glu
    210             215             220

Ile Ile Val Lys Ala Met Ser Asp Tyr Trp Val Val Gly Lys Lys Ser
225             230             235             240

Asp Arg Arg Glu Leu Tyr Val Ile Leu Asn Gln Lys Asn Ala Asn Leu
            245             250             255

Ile Glu Val Asn Glu Val Lys Lys Leu Cys Ala Thr Gln Phe Asn Asn
            260             265             270
```

Page 2

Ile Phe Phe Leu Asp
        275

<210> 2

<211> 543

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 28   protein

<400> 2

Phe Ala Val Asp Ala Lys Ala Leu Pro Gln Asn Lys Pro Arg Pro Leu
1   5   10   15

Thr Gln Glu Glu Ile Ala Gln Arg Arg Glu Arg Ala Arg Gln Arg His
            20   25   30

Ala Glu Lys Leu Ala Ala Ala Gln Gly Gln Ala Pro Leu Glu Pro Thr
        35   40   45

Gln Asp Gly Ser Ala Ile Glu Thr Cys Pro Lys Gly Asp Glu Pro Arg
        50   55   60

Gly Asp Glu Gln Gln Val Glu Ser Met Thr Pro Lys Pro Val Leu Gln
65   70   75   80

Glu Glu Asn Asn Gln Glu Ser Phe Ile Ala Phe Ala Arg Val Phe Ser
                85   90   95

Gly Val Ala Arg Arg Gly Lys Lys Ile Phe Val Leu Gly Pro Lys Tyr
            100   105   110

Ser Pro Leu Glu Phe Leu Arg Arg Val Pro Leu Cys Phe Ser Ala Pro
        115   120   125

Pro Asp Gly Leu Pro Gln Val Pro His Met Ala Tyr Cys Ala Leu Glu
    130   135   140

Asn Leu Tyr Leu Leu Met Gly Arg Glu Leu Glu Tyr Leu Glu Glu Val
145   150   155   160

Pro Pro Gly Asn Val Leu Gly Ile Gly Gly Leu Gln Asp Phe Val Leu
            165   170   175

```
Lys Ser Ala Thr Leu Cys Ser Leu Pro Ser Cys Pro Pro Phe Ile Pro
            180             185             190


Leu Asn Phe Glu Ala Thr Pro Ile Val Arg Val Ala Val Glu Pro Lys
            195             200             205


His Pro Ser Glu Met Pro Gln Leu Val Lys Gly Met Lys Leu Leu Asn
210             215             220


Gln Ala Asp Pro Cys Val Gln Ile Leu Ile Gln Glu Thr Gly Glu His
225             230             235             240


Val Leu Val Thr Ala Gly Glu Val His Leu Gln Arg Cys Leu Asp Asp
                245             250             255


Leu Lys Glu Arg Phe Ala Lys Ile His Ile Ser Val Ser Glu Pro Ile
            260             265             270


Ile Pro Phe Arg Glu Thr Ile Thr Lys Pro Pro Lys Val Asp Met Val
            275             280             285


Asn Glu Glu Ile Gly Lys Gln Gln Lys Val Ala Val Ile His Gln Met
    290             295             300


Lys Glu Asp Gln Ser Lys Ile Pro Glu Gly Ile Gln Val Asp Ser Asp
305             310             315             320


Gly Leu Ile Thr Ile Thr Thr Pro Asn Lys Leu Ala Thr Leu Ser Val
                325             330             335


Arg Ala Met Pro Leu Pro Glu Glu Val Thr Gln Ile Leu Glu Glu Asn
            340             345             350


Ser Asp Leu Ile Arg Ser Met Glu Gln Leu Thr Ser Ser Leu Asn Glu
            355             360             365


Gly Glu Asn Thr His Met Ile His Gln Lys Thr Gln Glu Lys Ile Trp
370             375             380


Glu Phe Lys Gly Lys Leu Glu Gln His Leu Thr Gly Arg Arg Trp Arg
385             390             395             400


Asn Ile Val Asp Gln Ile Trp Ser Phe Gly Pro Arg Lys Cys Gly Pro
            405             410             415


Asn Ile Leu Val Asn Lys Ser Glu Asp Phe Gln Asn Ser Val Trp Thr
            420             425             430
```
Page 4

Gly Pro Ala Asp Lys Ala Ser Lys Glu Ala Ser Arg Tyr Arg Asp Leu
        435   440   445

Gly Asn Ser Ile Val Ser Gly Phe Gln Leu Ala Thr Leu Ser Gly Pro
    450   455   460

Met Cys Glu Glu Pro Leu Met Gly Val Cys Phe Val Leu Glu Lys Trp
465   470   475   480

Asp Leu Ser Lys Phe Glu Glu Gln Gly Ala Ser Asp Leu Ala Lys Glu
            485   490   495

Asp Arg Arg Lys Met Lys Pro Val Leu Val Glu Met Lys Thr Lys Ser
        500   505   510

Tyr Lys Met Ala Ala Leu Arg Pro Leu Arg Arg Gly His His Arg Lys
        515   520   525

Glu Asn Leu His Ser Leu Thr Ala Met Asp Leu Ser Gln Asp Ser
    530   535   540

<210> 3

<211> 396

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 19

<400> 3

Met Lys Ala Val Lys Ser Glu Arg Glu Arg Gly Ser Arg Arg Arg His
1   5   10   15

Arg Asp Gly Asp Val Val Leu Pro Ala Gly Val Val Val Lys Gln Glu
            20   25   30

Arg Leu Ser Pro Glu Val Ala Pro Pro Ala His Arg Arg Pro Asp His
        35   40   45

Ser Gly Gly Ser Pro Ser Pro Pro Thr Ser Glu Pro Ala Arg Ser Gly
    50   55   60

His Arg Gly Asn Arg Ala Arg Gly Val Ser Arg Ser Pro Pro Lys Lys

65   70   75   80

Lys Asn Lys Ala Ser Gly Arg Arg Ser Lys Ser Pro Arg Ser Lys Arg
                85   90   95

Asn Arg Ser Pro His His Ser Thr Val Lys Val Lys Gln Glu Arg Glu
            100   105   110

Asp His Pro Arg Arg Gly Arg Glu Asp Arg Gln His Arg Glu Pro Ser
            115   120   125

Glu Gln Glu His Arg Arg Ala Arg Asn Ser Asp Arg Asp Arg His Arg
    130   135   140

Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro Gly Ser Gly
145   150   155   160

Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln Ala Gln Glu
                165   170   175

Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His Arg Gln Arg
            180   185   190

Asn Asp Val Gly Gly Gly Gly Ser Glu Ser Gln Glu Leu Val Pro Arg
            195   200   205

Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys Glu Lys Pro
    210   215   220

Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn Thr Phe Arg
225   230   235   240

Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg Ile Pro Lys
                245   250   255

Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val Leu Pro Val
            260   265   270

Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg His Arg Arg
            275   280   285

Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys Gln His Ala
    290   295   300

Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp Gly Thr Val
305   310   315   320

Page 6

```
Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser Gly Asn Gly
                325             330             335

Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr Tyr Glu Leu
            340             345             350

Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg Glu Tyr Val
            355             360             365

Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg Lys Asp Asp
        370             375             380

Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser
385             390             395
```

<210> 4

<211> 82

<212> PRT

<213> Unknown

<220>

<223> Protein Sequence of NIPP-1 domain homologous to SNIP 1

<400> 4

```
Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr Ile Asp His
1           5               10              15

Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu
            20              25              30

Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu
            35              40              45

Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp
        50              55              60

Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu
65              70              75              80

Lys Pro
```

<210> 5

<211> 255

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 19 Smad binding domain sequence

<400> 5

Arg His Arg Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro
1   5   10   15

Gly Ser Gly Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln
            20   25   30

Ala Gln Glu Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His
        35   40   45

Arg Gln Arg Asn Asp Val Gly Gly Gly Ser Glu Ser Gln Glu Leu
    50   55   60

Val Pro Arg Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys
65   70   75   80

Glu Lys Pro Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn
                85   90   95

Thr Phe Arg Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg
            100   105   110

Ile Pro Lys Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val
        115   120   125

Leu Pro Val Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg
    130   135   140

His Arg Arg Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys
145   150   155   160

Gln His Ala Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp
            165   170   175

Gly Thr Val Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser
            180   185   190

Gly Asn Gly Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr
    195   200   · 205

Tyr Glu Leu Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg
210   215   220

Glu Tyr Val Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg
225   230   235   240

Lys Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser
              245   250   255

<210> 6

<211> 163

<212> PRT

<213> Unknown

<220>

<223> clone S1 +19 protein

<400> 6

Gly Ala Leu Thr Glu Asp Thr Asn Thr Phe Arg Gly Val Val Ile Lys
1   5   10   15

Tyr Asn Glu Pro Pro Glu Ala Lys Lys Pro Asn Ala Arg Trp Arg Leu
              20   25   30

Tyr Pro Phe Lys Gly Glu Glu Ser Leu Gln Val Leu Tyr Ile His Arg
              35   40   45

Gln Ser Ala Tyr Leu Ile Gly Arg Asp His Lys Ile Ala Asp Ile Pro
              50   55   60

Val Asp His Pro Ser Cys Ser Lys Gln His Ala Val Leu Gln Phe Arg
65   70   75   80

Ser Met Pro Phe Thr Arg Asp Asp Gly Thr Lys Ala Arg Arg Ile Met
              85   90   95

Pro Tyr Ile Ile Asp Leu Gly Ser Gly Asn Gly Thr Phe Leu Asn Glu
              100   105   110

Lys Lys Ile Glu Pro Gln Arg Tyr Ile Glu Leu Gln Glu Lys Asp Met
              115   120   125

Leu Lys Phe Gly Phe Ser Thr Arg Glu Tyr Val Val Met Lys Glu Arg

```
                            130                     135                   140
Glu Ile Thr Glu Glu Glu Leu Ala Glu Gly Glu Asp Val Lys Lys Glu
145                     150                   155                   160

Glu Ser Asp
```

<210> 7

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 12 Protein

<400> 7

```
Glu Phe Gly Thr Arg Arg Met Met Glu Gly Leu Asp Asp Gly Pro Asp
1               5                   10                  15


Phe Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu
            20                  25                  30


Gln Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu
        35                  40                  45


Arg Asp Lys Val Lys Phe Thr Val His Thr Lys Ser Ser Leu Pro Asn
    50                  55                  60


Phe Lys Gln Asn Glu Phe Ser Val Val Arg Gln His Glu Glu Phe Ile
65                  70                  75                  80


Trp Leu His Asp Ser Phe Val Glu Asn Glu Asp Tyr Ala Gly Tyr Ile
            85                  90                  95


Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys
            100             105             110


Leu Gln Lys Leu Gly Glu Gly Glu Gly Ser Met Thr Lys Glu Glu Phe
            115             120             125


Thr Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys
            130             135             140
```

Lys Thr Val Ala Met His Glu Val Phe Leu Cys Arg Val Ala Ala His
145   150   155   160

Pro Ile Leu Arg Arg Asp Leu Asn Phe His Val Phe Leu Glu Tyr Asn
                165   170   175

Gln Asp Leu Ser Val Arg Gly Lys Lys Lys Lys Lys Asn Ser Arg Ser
                180   185   190

Phe Gly Leu Leu Arg Gln
            195

<210>   8

<211>   414

<212>   PRT

<213>   Unknown

<220>

<223>   Clone S1+12 -2 protein Sequence

<400>   8

His Ala Ser Gly Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly
1   5   10   15

Pro Asp Phe Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val
            20   25   30

Asp Leu Gln Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu
            35   40   45

Ser Glu Arg Asp Lys Val Lys Phe Thr Val His Thr Lys Ser Ser Leu
    50   55   60

Pro Asn Phe Lys Gln Asn Glu Phe Ser Val Val Arg Gln His Glu Glu
65   70   75   80

Phe Ile Trp Leu His Asp Ser Phe Val Glu Asn Glu Asp Tyr Ala Gly
                85   90   95

Tyr Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Asp Ala Ser Arg
                100   105   110

Glu Lys Leu Gln Lys Leu Gly Glu Gly Glu Gly Ser Met Thr Lys Glu
            115   120   125

Glu Phe Thr Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu Ala Ile
130   135   140

Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Cys Arg Val Ala
145   150   155   160

Ala His Pro Ile Leu Arg Arg Asp Leu Asn Phe His Val Phe Leu Glu
                165   170   175

Tyr Asn Gln Asp Leu Ser Val Arg Gly Lys Asn Lys Lys Glu Lys Leu
            180   185   190

Glu Asp Phe Phe Lys Asn Met Val Lys Ser Ala Asp Gly Val Ile Val
        195   200   205

Ser Gly Val Lys Asp Val Asp Asp Phe Phe Glu His Glu Arg Thr Phe
    210   215   220

Leu Leu Glu Tyr His Asn Arg Val Lys Asp Ala Ser Ala Lys Ser Asp
225   230   235   240

Arg Met Thr Arg Ser His Lys Ser Ala Ala Asp Asp Tyr Asn Arg Ile
            245   250   255

Gly Ser Ser Leu Tyr Ala Leu Gly Thr Gln Asp Ser Thr Asp Ile Cys
            260   265   270

Lys Phe Phe Leu Lys Val Ser Glu Leu Phe Asp Lys Thr Arg Lys Ile
    275   280   285

Glu Ala Arg Val Ser Ala Asp Glu Asp Leu Lys Leu Ser Asp Leu Leu
    290   295   300

Lys Tyr Tyr Leu Arg Glu Ser Gln Ala Ala Lys Asp Leu Leu Tyr Arg
305   310   315   320

Arg Ser Arg Ser Leu Val Asp Tyr Glu Asn Ala Asn Lys Ala Leu Asp
            325   330   335

Lys Ala Arg Ala Lys Asn Lys Asp Val Leu Gln Ala Glu Thr Ser Gln
        340   345   350

Gln Leu Cys Cys Gln Lys Phe Glu Lys Ile Ser Glu Ser Ala Lys Gln
        355   360   365

Glu Leu Ile Asp Phe Lys Thr Arg Arg Val Ala Ala Phe Arg Lys Asn
370   375   380

Page 12

Leu Val Glu Leu Ala Glu Leu Glu Leu Lys His Ala Lys Gly Asn Leu
385   390   395   400

Gln Leu Leu Gln Asn Cys Leu Ala Val Leu Asn Gly Asp Thr
              405   410

<210> 9

<211> 294

<212> PRT

<213> Unknown

<220>

<223> Clone S1+12 -5 protein

<400> 9

Met Thr Thr Leu Thr Glu Ile Lys Leu Leu Pro Ser Leu Val Leu Leu
1   5   10   15

Val Cys Cys Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
              20   25   30

Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
          35   40   45

Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
      50   55   60

Gly Lys Asn Lys Lys Glu Lys Leu Glu Asp Phe Phe Lys Asn Met Val
65   70   75   80

Lys Ser Ala Asp Gly Val Ile Val Ser Gly Val Lys Asp Val Asp Asp
              85   90   95

Phe Phe Glu His Glu Arg Thr Phe Leu Leu Glu Tyr His Asn Arg Val
          100   105   110

Lys Asp Ala Ser Ala Lys Ser Asp Arg Met Thr Arg Ser His Lys Ser
          115   120   125

Ala Ala Asp Asp Tyr Asn Arg Ile Gly Ser Ser Leu Tyr Ala Leu Gly
      130   135   140

Thr Gln Asp Ser Thr Asp Ile Cys Lys Phe Phe Leu Lys Val Ser Glu
                            Page 13

```
      145                    150                    155                    160

Leu Phe Asp Lys Thr Arg Lys Ile Glu Ala Arg Val Ser Ala Asp Glu
            165                     170                 175

Asp Leu Lys Leu Ser Asp Leu Leu Lys Tyr Tyr Leu Arg Glu Ser Gln
            180                     185                 190

Ala Ala Lys Asp Leu Leu Tyr Arg Arg Ser Arg Ser Leu Val Asp Tyr
            195                 200                 205

Glu Asn Ala Asn Lys Ala Leu Asp Lys Ala Arg Ala Lys Asn Lys Asp
        210                 215                 220

Val Leu Gln Ala Glu Thr Ser Gln Gln Leu Cys Cys Gln Lys Phe Glu
225                     230                 235                     240

Lys Ile Ser Glu Ser Ala Lys Gln Glu Leu Ile Asp Phe Lys Thr Arg
            245                     250                 255

Arg Val Ala Ala Phe Arg Lys Asn Leu Val Glu Leu Ala Glu Leu Glu
            260                 265                     270

Leu Lys His Ala Lys Gly Asn Leu Gln Leu Leu Gln Asn Cys Leu Ala
            275                 280                     285

Val Leu Asn Gly Asp Thr
            290
```

<210> 10

<211> 989

<212> DNA

<213> Unknown

<220>

<223> Clone S3-1 DNA Sequence. Called tumor associated gene in homo sap
      iens, unknown function

<220>

<221> misc_feature

<222> (1)..(989)

<223> n can be any nucleotide

<400> 10

```
atgtcaagtg gaatttggca gagaggcaaa gaagaagaag gagtttatgg ttttctaata      60

gaagatatca ggaaggaagt gaatagagct tctaaactga aatgctgtgt ttgcaagaaa     120

aatggtgctt caattggatg tgttgcaccc cgatgtaaac gaagttatca tttcccatgt     180

ggacttcaga gagaatgtat tttccagttt actggcaatt ttgcgtcatt ttgttgggac     240

catcgacctg ttcaaataat tacatctaat aattatagag agtccttacc atgcaccatt     300

tgcttggaat ttattgagcc tattccaagt tataacatat tacgaagtcc ttgttgtaag     360

aacgcttggt ttcatagaga ctgtttacag gttcaagcaa taaatgcggg agtgtttttc     420

tttaggtgta caatatgcaa taatagtgac atctttcaga aagagatgtt gagaatggga     480

attcatattc ctgaaaaaga tgcttcctgg gaattagagg aaaacgctta tcaagagctt     540

ctgcagcact atgagcgttg tgatgttcga agatgtcgtt gcaaagaagg gcgagactat     600

aatgcacctg atagcaaatg ggaaataaag cgctgtcagt gttgtggttc cagtggcaca     660

catttagcct gctcctcatt acggtcatgg gagcaaaatt gggagtgttt ggaatgtagg     720

ggtattatct acaattcagg agagttccaa acagccaaaa aacatgtatt acccaattct     780

aataatgtgg ggattacaga ttgtttgttg gaagagtcat cacctaaatt acccagacag     840

tcacctggat cccagagtaa agatctactg aggcaaggca gcaaatttag aagaaatgta     900

tcaacactat aatagagtt aggattccaa attaaaaaaa aaaaaaaaaa actcgagaag     960

nttggantnt tcgccagagg tttggtcaa                                      989
```

<210> 11

<211> 329

<212> PRT

<213> Unknown

<220>

<223>   Clone S3-1 protein Sequence

<220>

<221> MISC_FEATURE

<222> (1)..(329)

<223> X can be any amino acid

<400> 11

Met Ser Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Tyr
1   5   10   15

Gly Phe Leu Ile Glu Asp Ile Arg Lys Glu Val Asn Arg Ala Ser Lys
              20   25   30

Leu Lys Cys Cys Val Cys Lys Lys Asn Gly Ala Ser Ile Gly Cys Val
          35   40   45

Ala Pro Arg Cys Lys Arg Ser Tyr His Phe Pro Cys Gly Leu Gln Arg
      50   55   60   .

Glu Cys Ile Phe Gln Phe Thr Gly Asn Phe Ala Ser Phe Cys Trp Asp
65   70   75   80

His Arg Pro Val Gln Ile Ile Thr Ser Asn Asn Tyr Arg Glu Ser Leu
              85   90   95

Pro Cys Thr Ile Cys Leu Glu Phe Ile Glu Pro Ile Pro Ser Tyr Asn
              100   105   110

Ile Leu Arg Ser Pro Cys Cys Lys Asn Ala Trp Phe His Arg Asp Cys
          115   120   125

Leu Gln Val Gln Ala Ile Asn Ala Gly Val Phe Phe Phe Arg Cys Thr
      130   135   140

Ile Cys Asn Asn Ser Asp Ile Phe Gln Lys Glu Met Leu Arg Met Gly
145   150   155   160

Ile His Ile Pro Glu Lys Asp Ala Ser Trp Glu Leu Glu Glu Asn Ala
              165   170   175

Tyr Gln Glu Leu Leu Gln His Tyr Glu Arg Cys Asp Val Arg Arg Cys
          180   185   190

Arg Cys Lys Glu Gly Arg Asp Tyr Asn Ala Pro Asp Ser Lys Trp Glu
          195   200   205

Ile Lys Arg Cys Gln Cys Cys Gly Ser Ser Gly Thr His Leu Ala Cys
      210   215   220

Ser Ser Leu Arg Ser Trp Glu Gln Asn Trp Glu Cys Leu Glu Cys Arg
225   230   235   240

Gly Ile Ile Tyr Asn Ser Gly Glu Phe Gln Thr Ala Lys Lys His Val
          245   250   255

Page 16

```
Leu Pro Asn Ser Asn Asn Val Gly Ile Thr Asp Cys Leu Leu Glu Glu
        260             265             270


Ser Ser Pro Lys Leu Pro Arg Gln Ser Pro Gly Ser Gln Ser Lys Asp
        275             280             285


Leu Leu Arg Gln Gly Ser Lys Phe Arg Arg Asn Val Ser Thr Leu Leu
    290             295             300


Ile Glu Leu Gly Phe Gln Ile Lys Lys Lys Lys Lys Leu Glu Lys
305             310             315             320


Xaa Gly Xaa Phe Ala Arg Gly Leu Val
            325
```

<210> 12

<211> 1673

<212> DNA

<213> Unknown

<220>

<223> Clone S3-12 DNA sequence

<400> 12

```
aggaaagcta cagaaattag cactgcagtg gttcagaggt cagctaccat tggcagttct     60

ccagttctct atagccagtc agctatagct acaggtcacc aggcagcagg gattggaaac    120

caggcaacag gaattggaca tcagacaata ccagttagcc ttccagcagc aggaatgggt    180

catcaggcca gaggaatgag cctgcagtca aattaccttg gactagcggc agcacctgca    240

attatgagtt atgcagaatg ttctgtccca attggagtga ctgctccctc attgcagcca    300

gttcaggccc gaggtgctgt gcctaccgct accattatag aaccaccacc accacctcct    360

cctcctcctc tccaccacc accagctccc aaaatgccac cacctgaaaa gacaaaaaaa    420

ggaaggaaag acaaggcaaa gaagagtaag accaaaatgc catctttggt aaaaaagtgg    480

cagagtatcc agcgtgagtt agatgaagag gacaattcta gttccagtga agaggatcgg    540

gaatcaactg cacagaagcg aattgaagag tggaaacagc agcagctggt tagtggcatg    600

gcagagagaa atgctaattt tgaagccctt cctgaggatt ggagagcaag gctgaagaga    660

aggaaaatgg ctccaaacac atagttttta agtttttaaa actttttgt attattgttt    720

gttttgtgtt cagttcaaag tcttaaccag ttttattgtc aaataaacta taaatgttat    780

ggggggagatc ttataaattt cctgggcaag agtgtatgca tacaaagttt tcacttttgt    840
```

```
gaaatgtaat ttttctgttt ttgcaaaggg atgaggtgat tggaattgct ttgaccatgc      900

tgcctttatt ctcaaactgg caaacttagc atgttaggtg tattaacctc atcagtcttg      960

aagaacatgt ggctcatgag tataacactt ctgtagagga ctccctgaca aaagtgaaga     1020

attaacttct cctccagaac aagtgcaatt cagaaggcag ctctgcattc taccttgctt     1080

gactggaatt gtctgaagct ttttctggcc tcttttctct agtcggccac ccctgaagtg     1140

ctgaggtcta agtggtttac ctcgtgctga tagatggcca cactctttag agtagttctc     1200

ataagttcta gaactggtag ctcggtcgtt tcgcacacta ggtggcatac aggcagcagc     1260

aggtgttcat atccttgatt ttgagaattt cccctcaagt atgtggcagt aaatacaaca     1320

agacactcta tgtattaatg tctccattgt cttaaccctg ttccaaaaca aaattcacct     1380

cctttcttta tgtgaatgta ttctccataa aattccagta tttaaaaagc agtttactgt     1440

tctgtacttt ctgttgtatc acaatcaggt aaaagtcact ttaaactgag gaaacggcaa     1500

attgtgtttt aaagctcttt gtatttctcc agtttctgac cttgtaaatt tgtatatatg     1560

cactaataaa gcttttttta taatcctgaa aaaaaaaaaa aaaaaaaaaa aaaactcgag     1620

aagctttgga cttcttcgcc agaggtttgg tcaagtctcc aatcaaggtt gtc           1673
```

<210> 13

<211> 233

<212> PRT

<213> Unknown

<220>

<223> Clone S3 +12 protein

<400> 13

```
Glu Phe Gly Thr Arg Arg Arg Lys Ala Thr Glu Ile Ser Thr Ala Val
1               5                   10                  15

Val Gln Arg Ser Ala Thr Ile Gly Ser Ser Pro Val Leu Tyr Ser Gln
            20                  25                  30

Ser Ala Ile Ala Thr Gly His Gln Ala Ala Gly Ile Gly Asn Gln Ala
        35                  40                  45

Thr Gly Ile Gly His Gln Thr Ile Pro Val Ser Leu Pro Ala Ala Gly
    50                  55                  60

Met Gly His Gln Ala Arg Gly Met Ser Leu Gln Ser Asn Tyr Leu Gly
```

Page 18

Leu Ala Ala Ala Pro Ala Ile Met Ser Tyr Ala Glu Cys Ser Val Pro
            85   90   95

Ile Gly Val Thr Ala Pro Ser Leu Gln Pro Val Gln Ala Arg Gly Ala
            100   105   110

Val Pro Thr Ala Thr Ile Ile Glu Pro Pro Pro Pro Pro Pro Pro Pro
            115   120   125

Pro Pro Pro Pro Pro Pro Ala Pro Lys Met Pro Pro Pro Glu Lys Thr
    130   135   140

Lys Lys Gly Arg Lys Asp Lys Ala Lys Lys Ser Lys Thr Lys Met Pro
145   150   155   160

Ser Leu Val Lys Lys Trp Gln Ser Ile Gln Arg Glu Leu Asp Glu Glu
            165   170   175

Asp Asn Ser Ser Ser Ser Glu Glu Asp Arg Glu Ser Thr Ala Gln Lys
            180   185   190

Arg Ile Glu Glu Trp Lys Gln Gln Gln Leu Val Ser Gly Met Ala Glu
            195   200   205

Arg Asn Ala Asn Phe Glu Ala Leu Pro Glu Asp Trp Arg Ala Arg Leu
    210   215   220

Lys Arg Arg Lys Met Ala Pro Asn Thr
225   230

<210>   14

<211>   926

<212>   DNA

<213>   Unknown

<220>

<223>   Clone S3 + 103 DNA sequence

<400>   14
gaattcggca cgaggcggac gtcattgagc tgcgaccctt gttcaacgcc gttgggcaag   60

ccagctgctg gaggtgccga gaatctgagt ttcggcaagc agccaggtct ggaaactaat   120

attttaaaaa tgactacacc aaacaagaca cctcctggtg ctgaccccaa gcagttggaa   180

```
aggactggaa cagtacggga aattgggtca caagctgttt ggtcactctc atcttgcaaa    240

ccaggatttg gagtggatca gttacgagat gacaatctag aaacttattg gcaatcagat    300

ggttcccagc ctcatttagt gaacatccaa ttcagaagaa aaacaacagt gaagacatta    360

tgtatttatg cagactacaa atctgatgaa agctatactc caagcaagat ctcagtcaga    420

gtaggaaata attttcacaa ccttcaagaa attcggcaac ttgagttggt ggaaccaagt    480

ggctggattc atgttccctt aactgacaat cataagaagc caactcgtac attcatgata    540

cagattgctg ttctagccaa tcaccagaat ggaagagaca cccatatgag acaaattaaa    600

atatacacac cagtagaaga gagctccatt ggtaaatttc ctagatgtac aactatagat    660

ttcatgatgt atcgttcaat aaggtgactt taaaatgaga cgaaaatcat taaacgtatc    720

tttgttctta tcctgtattt aaataatata tcatgtacct ttattgaaca aggcatccgt    780

tatatctaat tttgtatatg tttaaaaata ttttattgta actttgacaa ataaatttgg    840

ggtcatatta tctttatttt ctttaacatg taataaagct cacatatttt acattaaaaa    900

aaaaaaaaaa aaaaaaactc gagaag                                         926
```

<210> 15

<211> 301

<212> PRT

<213> Unknown

<220>

<223> Clone S3 + 103 prtoein Sequence

<400> 15

```
Glu Phe Gly Thr Arg Arg Thr Ser Leu Ser Cys Asp Pro Cys Ser Thr
1               5                  10                  15


Pro Leu Gly Lys Pro Ala Ala Gly Gly Ala Glu Asn Leu Ser Phe Gly
                20                  25                  30


Lys Gln Pro Gly Leu Glu Thr Asn Ile Leu Lys Met Thr Thr Pro Asn
            35                  40                  45


Lys Thr Pro Pro Gly Ala Asp Pro Lys Gln Leu Glu Arg Thr Gly Thr
        50                  55                  60


Val Arg Glu Ile Gly Ser Gln Ala Val Trp Ser Leu Ser Ser Cys Lys
65                  70                  75                  80
```

```
Pro Gly Phe Gly Val Asp Gln Leu Arg Asp Asp Asn Leu Glu Thr Tyr
                85                  90                  95

Trp Gln Ser Asp Gly Ser Gln Pro His Leu Val Asn Ile Gln Phe Arg
           100             105                 110

Arg Lys Thr Thr Val Lys Thr Leu Cys Ile Tyr Ala Asp Tyr Lys Ser
           115             120             125

Asp Glu Ser Tyr Thr Pro Ser Lys Ile Ser Val Arg Val Gly Asn Asn
       130             135             140

Phe His Asn Leu Gln Glu Ile Arg Gln Leu Glu Leu Val Glu Pro Ser
145             150             155             160

Gly Trp Ile His Val Pro Leu Thr Asp Asn His Lys Lys Pro Thr Arg
               165             170             175

Thr Phe Met Ile Gln Ile Ala Val Leu Ala Asn His Gln Asn Gly Arg
           180             185             190

Asp Thr His Met Arg Gln Ile Lys Ile Tyr Thr Pro Val Glu Glu Ser
       195             200             205

Ser Ile Gly Lys Phe Pro Arg Cys Thr Thr Ile Asp Phe Met Met Tyr
   210             215             220

Arg Ser Ile Arg Leu Asn Glu Thr Lys Ile Ile Lys Arg Ile Phe Val
225             230             235             240

Leu Ile Leu Tyr Leu Asn Asn Ile Ser Cys Thr Phe Ile Glu Gln Gly
           245             250             255

Ile Arg Tyr Ile Phe Cys Ile Cys Leu Lys Ile Phe Tyr Cys Asn Phe
           260             265             270

Asp Lys Ile Trp Gly His Ile Ile Phe Ile Phe Phe Asn Met Ser Ser
           275             280             285

His Ile Leu His Lys Lys Lys Lys Lys Lys Asn Ser Arg
   290             295             300
```

<210> 16

<211> 844

<212> DNA

Page 21

<213>   Unknown

<220>

<223>   Clone S3 + 125 DNA Sequence

<220>

<221>   misc_feature

<222>   (1)..(844)

<223>   n can be any nucleotide

<400>   16

```
caggaatctg tccgaagata attgaggcag aagagtccag aatgggcctc atcatcgtca     60
atgcctggta cgggaacttt gtcaatgaca agagcaggaa gagcgagaag gtgaaggtga    120
ttgacgtgac tgtgccctgc agtgcctggg taaggactcg aagctcatcc tcacgaggcc    180
tccaagctgg gctgcctggc ttttatgacc cgtgtgtggg ggaagagaag aacctgaaag    240
tgctctatca gttccggggc gtcctgcatc aggtgatggt gctggacagt gaggccctcc    300
ggataccaaa gcagtcccac aggatcgata cagatggata aactgccaag aaccagattt    360
ttaaaaggcc gcaaaaaatc ttttcctggg agtctacaaa tttggaaatg aaaaaaccca    420
gacatcagat gtttttattt tatattatta ttatagaagg tggtaccatt atcaattatg    480
tgaagggaca tgcagacacc ccagcactgg tatctgagta acggctaaga acctccttcc    540
tctggttttg aaaagcagtt cgggttgtcc aattctgtaa cattcatctc cattttttaa    600
aaaggtttct ctgacggccc cacggcccga gccgcggtga gcgtcgtgtt gcatgagcct    660
gggcccgggg cttcccgtgc gcctctgccg caggtgcttc tgggcaccca tcctctgcgt    720
ttcatttgca gtcgactgta cagaaggcac tcaccacaat aaacctttcc tgaaagcaaa    780
aaaaaaaaaa aaaaaactcg agaaggtttg gacttgttcg ccagaggttt ggtcaagtnt    840
ccaa                                                                 844
```


<210>   17

<211>   118

<212>   PRT

<213>   Unknown

<220>

<223>   Clone S3 + 125 Protein Sequence

<400> 17

Ile Arg His Glu Ala Ala Gly Ile Cys Pro Lys Ile Ile Glu Ala Glu
1   5   10   15

Glu Ser Arg Met Gly Leu Ile Ile Val Asn Ala Trp Tyr Gly Asn Phe
            20   25   30

Val Asn Asp Lys Ser Arg Lys Ser Glu Lys Val Lys Val Ile Asp Val
        35   40   45

Thr Val Pro Cys Ser Ala Trp Val Arg Thr Arg Ser Ser Ser Ser Arg
    50   55   60

Gly Leu Gln Ala Gly Leu Pro Gly Phe Tyr Asp Pro Cys Val Gly Glu
65   70   75   80

Glu Lys Asn Leu Lys Val Leu Tyr Gln Phe Arg Gly Val Leu His Gln
            85   90   95

Val Met Val Leu Asp Ser Glu Ala Leu Arg Ile Pro Lys Gln Ser His
            100   105   110

Arg Ile Asp Thr Asp Gly
            115

<210> 18

<211> 216

<212> DNA

<213> Unknown

<220>

<223> Clone S1 + 30 DNA Sequence

<400> 18
gaattcggca cgaggcggac aaagggaatc aaagttgtgg gaaaatggaa ggaagtgaag   60

attgacccaa atatgtttgc agatggacag atggatgact tggtgtgctt tgaggaattg   120

acagattacc agttggtctc ccctgccaag aattccctcc agctctcttc tcaaaggaag   180

cacccaagag aaaggcacaa gctgtttcag aagaag   216

<210> 19

<211> 72

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 30 Protein Sequence

<400> 19

```
Glu Phe Gly Thr Arg Arg Thr Lys Gly Ile Lys Val Val Gly Lys Trp
1               5               10              15

Lys Glu Val Lys Ile Asp Pro Asn Met Phe Ala Asp Gly Gln Met Asp
            20              25              30

Asp Leu Val Cys Phe Glu Glu Leu Thr Asp Tyr Gln Leu Val Ser Pro
        35              40              45

Ala Lys Asn Ser Leu Gln Leu Ser Ser Gln Arg Lys His Pro Arg Glu
    50              55              60

Arg His Lys Leu Phe Gln Lys Lys
65                  70
```

<210> 20

<211> 261

<212> DNA

<213> Unknown

<220>

<223> Clone S3+14 5' DNA sequence

<400> 20

```
cgatttctag cgtatatgga ggatcgcaga aaacagaagt ggcaaagatg taaaaaaaat      60

aataaggcag aattgaactg tttgggaatg gaaccagtac agacagctaa ctctagaaat     120

gggaaaaagg gtcatcacac tgaaacggtg ttcaaccggg ttttgccagg gcctattgca     180

ccagagagca gcaagaagcg gcccgtagat gcgaccagac ctttctaaga tgatggccct     240

catgcaggtg gaagcatcgg t                                               261
```

<210> 21

<211> 547

<212> DNA

<213> Unknown

<220>

<223> Clone S3+14 3' DNA sequence

<400> 21
agaggccctc atgcagggtg gaagcactgg gtctctatct ctgcataaca cgttccaaca   60

cagcagtagt ggcctacagt ctgtgtcatc tttgggtcac agcagtgcca cttctgcatc   120

tttgcctttt atgccatttg tgatgggtgg tgcaccatca tcccctcatg tagactccag   180

caccatgctt catcaccacc accaccaccc ccaccccac catcaccacc atcaccatcc   240

aggcttgaga gcccctggct acccctcttc accagtgact accgcctctg gtactacctt   300

gcggttgcca ccactgcaac ctgaggagga tgacgatgag gatgaagaag atgatgatga   360

cttatctcag ggctatgata gctcagaaag ggacttctca ctcattgatg atcctatgat   420

gccagctaac tcagactcca gtgaagatgc tgatgactga gccccagca tgggcccat   480

tgcttgggcg gctgctgtat tttcatttac tctggccctt ggactatgga aacgtgggag   540

gggcagg   547

<210> 22

<211> 152

<212> PRT

<213> Unknown

<220>

<223> Clone S3+14 protein sequence

<400> 22

Glu Ala Leu Met Gln Gly Gly Ser Thr Gly Ser Leu Ser Leu His Asn
1   5   10   15

Thr Phe Gln His Ser Ser Ser Gly Leu Gln Ser Val Ser Ser Leu Gly
            20   25   30

His Ser Ser Ala Thr Ser Ala Ser Leu Pro Phe Met Pro Phe Val Met
            35   40   45

Gly Gly Ala Pro Ser Ser Pro His Val Asp Ser Ser Thr Met Leu His
    50   55   60

```
His His His His His Pro His Pro His His His His His His His Pro
65                  70              75                  80


Gly Leu Arg Ala Pro Gly Tyr Pro Ser Ser Pro Val Thr Thr Ala Ser
                85              90                  95


Gly Thr Thr Leu Arg Leu Pro Pro Leu Gln Pro Glu Glu Asp Asp Asp
            100             105             110


Glu Asp Glu Glu Asp Asp Asp Asp Leu Ser Gln Gly Tyr Asp Ser Ser
        115             120             125


Glu Arg Asp Phe Ser Leu Ile Asp Asp Pro Met Met Pro Ala Asn Ser
    130             135             140


Asp Ser Ser Glu Asp Ala Asp Asp
145             150
```

<210> 23

<211> 2496

<212> DNA

<213> Unknown

<220>

<223> Clone s1+19 cDNA sequence

<400> 23

```
gaggagctca actgatctgt tttctttcgc ccagccaaaa tcacagaatg aaggcggtga      60

agagcgaacg ggagcgaggg agccggcgaa gacaccggga cggggacgtg gtgctgccgg     120

cggggggtggt ggtgaagcag gagcgtctca gcccagaagt cgcacctccc gcccaccgcc     180

gtccggacca ctccggtggt agcccgtctc cgccgaccag cgagccggcc cgctcgggcc     240

accgcgggaa ccgagcccga ggagttagcc ggtccccacc caaaaagaaa aacaaggcct     300

cagggagaag aagcaagtct cctcgcagta agagaaaccg aagtcctcac cactcaacag     360

tcaaagtgaa gcaggagcgt gaggatcatc cccggagagg acgggaggat cggcagcaca     420

gggaaccatc agaacaggaa cacaggagag ctaggaacag tgaccgggac agacaccggg     480

gccattccca ccaaaggaga acgtctaacg agaggcctgg gagtgggcag ggtcagggac     540

gggatcgaga cactcagaac ctgcaggctc aggaagaaga gcgggagttt tataatgcca     600

ggcgacggga gcatcgccag aggaatgacg ttggtggtgg cggcagtgag tctcaggagt     660

tggttcctcg gcctggtggc aacaacaaag aaaaagaggt gcccgctaaa gaaaaaccaa     720
```

```
gctttgaact ttctggggca cttcttgagg acaccaacac tttccggggt gtagtcatta    780

aatatagtga gcccccagaa gcacgtatcc ccaaaaaacg gtggcgtctc tacccattta    840

aaaatgatga ggtgcttcca gtcatgtaca tacatcgaca gagtgcgtac ctactgggtc    900

gacaccgccg cattgcagac attccaattg atcacccgtc ttgttcaaag cagcatgcgg    960

tctttcaata tcggcttgtg gaatataccc gtgctgatgg cacagttggc cgaagagtga   1020

agccctacat cattgacctt ggctcaggca atggaacctt cttaaacaac aaacgtattg   1080

agccacagag atactatgaa ctaaaagaaa aggatgtact caaatttgga ttcagtagca   1140

gagaatacgt cttgctccat gagtcgtcgg acacttctga aatagacagg aaagatgacg   1200

aggatgagga ggaggaggaa gaagtgtctg acagctagca aactaagaac ccaaactatt   1260

gatacacggt ttccttcttg gaagtctttg attgactcag agagcactat ggtggtgggt   1320

ccagcactat ggtgctctct gtaatgcctc ttactgcctt aagtctttcc tctgttgctg   1380

accagattgt gttaccattt gaatacactg actaatgttt gttaaacttt ttctgtggca   1440

ccttggccac atgcctgcag gcatttgttt tcagaacagt ctcaccaatt acaacacacc   1500

gtgttttagt agaagtgttg tggttttagt tggtgctttc agaactgctg cctaggaaac   1560

tataaaccct tggttaaggg gaaatcatgg cttgttctct ttgtacagtt actttattta   1620

tataggtgtt aagctttgtg gaccaggtgt ttttcttttg gggcgaaccc ctgagcagag   1680

aatcttacta ggctttggtt atcaccaaaa caacctccag tatataccaa agctttgact   1740

tgtttgagct cttgagctta gaagttgatt ttgcacttat tttttggggg ggtgggaatg   1800

tactgcagtc agtaaacatt attgactgtt taacttaaac agatgcttta tggcacctgc   1860

tcaagcccgt gactgtacag aaggatcctg gttgctacca gtgggtgctg attcagcatc   1920

acaagtgact gaaattggct gtggatctgt tctttgtgaa agaattcctg atttctccat   1980

ggagcatgta cacaacaatt ttgatcatat taactgtact tcagttttgc attttttattc   2040

aaatgttatc tcttttttc tttgagaaat aaactgtcac tgatgtgaca gcgttctttc   2100

tttattctaa taacatgtat agatctaaag caggttgtgt tgtttacatg tttctacaca   2160

tttcatcctt taaaaagttg ttgagagagg ttgtatttac cttcccaagg ttggaaagca   2220

ggggaatttc ccagtgtcct agttttccac cagaggaata tgtgtaagta gcaaagtatt   2280

tgctgcttac atatagtgtg tatgtatgta tatatgtaaa ttgtgtgtta aagagctgat   2340

actgattttc atatgacaat gttaggcaaa ggcctccctg catttgaaga gcaggttttc   2400

atttatatgt atttttggga taaaaaaata aaatttgtaa atatagcccc caaaaaaaaa   2460

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                             2496
```

<210> 24

<211> 1965

<212> DNA

<213> Unknown

<220>

<223> Clone S1+12-2 cDNA sequence

<400> 24

```
cccacgcgtc cggcctcgga gcagccatga tggaaggcct ggacgacggc ccggacttcc    60

tctcagaaga ggaccgcgga cttaaagcaa taaatgtaga tcttcaaagt gatgctgctc   120

tgcaggtgga catttctgat gctcttagtg agcgggataa agtaaaattc actgttcaca   180

caaagagttc attgccaaat tttaaacaaa acgagttttc agttgttcgg caacatgagg   240

aatttatctg gcttcatgat tcctttgttg aaaatgaaga ctatgcaggt tatatcattc   300

caccagcacc accaagacct gattttgatg cttcaaggga aaaactacag aagcttggtg   360

aaggagaagg gtcaatgacg aaggaagaat tcacaaagat gaaacaggaa ctggaagctg   420

aatatttggc aatattcaag aagacagttg cgatgcatga agtgttcctg tgtcgtgtgg   480

cagcacatcc tattttgaga agagatttaa atttccatgt cttcttggaa tataatcaag   540

atttgagtgt gcgaggaaaa aataaaaaag agaaacttga agacttcttt aaaaacatgg   600

ttaaatcagc agatggagta atcgtttcag gagtaaagga tgtagatgat ttctttgagc   660

acgaacgaac atttcttttg gagtatcata accgagttaa ggatgcatct gctaaatctg   720

atagaatgac aagatcccac aaaagtgctg cagatgatta caatagaatt ggttcttcat   780

tatatgcttt aggaactcag gattctacag atatatgcaa gtttttctc aaagtttcag   840

aactgttcga taaaacaaga aaaatagaag cacgagtgtc tgctgatgaa gacctcaaac   900

tttctgatct tttaaaatat tacttaagag aatctcaagc tgctaaggat ctcctgtatc   960

gaaggtctag gtcactagtg gattatgaaa atgctaataa agcactggat aaagcaagag  1020

caaaaaataa agatgttcta caggccgaaa cttcccaaca attatgttgt cagaaatttg  1080

aaaaaatatc tgagtctgca aaacaagaac ttatagattt taagacaaga agagttgctg  1140

cattcagaaa aaatttagtg gaactggcag agttagaact gaagcatgca aagggtaatc  1200

tacagttgct gcagaactgc ctggcagtgt aaatggaga cacataagcc acactccgcc  1260

ttcctgttaa aaagggctgc cttccttcaa attttatttt tgttttctta atgatgttaa  1320

gcatttatgc tcactggaaa caaacaaaaa gcagctgaaa aagtgcatca actcctcttt  1380

ttctgagaaa catggagcag cgcacgccca ggcgatgcca gtctgtgtgc cgtgatgccg  1440

cactgtgttc cccatgacag tggtccatca tcgtgcactc gtcatactca gaagtccaaa  1500
```

```
gttcattctt ctttaaagta gcctctataa ctctgtttat tttataaata gtattcctta   1560

tggctgccac tcttatttac ctttaaataa tttctgaaat ttaacctttt cagaatgcat   1620

tgttgaaaca agataaagat tgcctttttt gaattttta aattttgttt ttaaaagcat   1680

ataccacctt agttcattca tgtatcctgg taaagcatct taatcagact tattttttaat  1740

tactgaatat ttcttagacg ttttgggaca gattttatgt aatctttata agtatgattt   1800

ctgaagaaaa gcaaatgcat tagtatgttt gccttaaact tgtagactaa accaagtatt   1860

gtaaaataaa cagcgataac agtgatagtt tttaactcta tggtcattgt atcactctgg   1920

aaaatgtgga gtagctgtaa taaatctact cctgtattat gcttt              1965
```

<210>   25

<211>   2269

<212>   DNA

<213>   Unknown

<220>

<223>   Clone S1+12-5 cDNA sequence

<400>   25
```
gcggcgccga gtcccgggag cgcggtgggg gcagcgggcg cggggcgggc gcggggaccg    60

cgccagcctg tcactaatgt ctccctttgt gtctccccca tctcatcctt ttccccggcg   120

cgccgtgccc gccgacccca caggaaggcc tggacgacgg cccggacttc ctctcagaag   180

aggaccgcgg acttaaagca ataaatgtag atcttcaaag tgatgctgct ctgcaggtgg   240

acatttctga tgctcttagt gagcgggata aagtaaaatt cactgttcac acaaagagtt   300

cattgccaaa ttttaaacaa aacgagtttt cagttgttcg gcaacatgag gaatttatct   360

ggcttcatga ttcctttgtt gaaaatgaag actatgcagg ttatatcatt ccaccagcac   420

caccaagacc tgattttgat gcttcaaggg aaaaactaca gaagcttggt gaaggagaag   480

ggtcaatgac gaaggaagaa ttcacaaaga tgaaacagga actggaagcg ggttggataa   540

cagagaacct tgggtttatt ctactgctac ctccatcctc tgcatccttc ttttttgtct   600

tcactgaatg actaccctca cagagatcaa acttctccca tcattggtcc tgctggtttg   660

ctgtgaatat ttggcaatat tcaagaagac agttgcgatg catgaagtgt tcctgtgtcg   720

tgtggcagca catcctattt tgagaagaga tttaaatttc catgtcttct tggaatataa   780

tcaagatttg agtgtgcgag gaaaaaataa aaaagagaaa cttgaagact tctttaaaaa   840

catggttaaa tcagcagatg gagtaatcgt ttcaggagta aaggatgtag atgatttctt   900

tgagcacgaa cgaacatttc ttttggagta tcataaccga gttaaggatg catctgctaa   960
```
Page 29

```
atctgataga atgacaagat cccacaaaag tgctgcagat gattacaata gaattggttc    1020

ttcattatat gctttaggaa ctcaggattc tacagatata tgcaagtttt ttctcaaagt    1080

ttcagaactg ttcgataaaa caagaaaaat agaagcacga gtgtctgctg atgaagacct    1140

caaactttct gatcttttaa aatattactt aagagaatct caagctgcta aggatctcct    1200

gtatcgaagg tctaggtcac tagtggatta tgaaaatgct aataaagcac tggataaagc    1260

aagagcaaaa aataaagatg ttctacaggc cgaaacttcc caacaattat gttgtcagaa    1320

atttgaaaaa atatctgagt ctgcaaaaca agaacttata gattttaaga caagaagagt    1380

tgctgcattc agaaaaaatt tagtggaact ggcagagtta gaactgaagc atgcaaaggg    1440

taatctacag ttgctgcaga actgcctggc agtgttaaat ggagacacat aagccacact    1500

ccgccttcct gttaaaaagg gctgccttcc ttcaaatttt atttttgttt tcttaatgat    1560

gttaagcatt tatgctcact ggaaacaaac aaaaagcagc tgaaaaagtg catcaactcc    1620

tctttttctg agaaacatgg agcagcgcac gcccaggcga tgccagtctg tgtgccgtga    1680

tgccgcactg tgttccccat gacagtggtc catcatcgtg cactcgtcat actcagaagt    1740

ccaaagttca ttcttcttta aagtagcctc tataactctg tttattttat aaatagtatt    1800

ccttatggct gccactctta tttaccttta aataatttct gaaatttaac cttttcagaa    1860

tgcattgttg aaacaagata aagattgcct tttttgaatt ttttaaattt tgtttttaaa    1920

agcatatacc accttagttc attcatgtat cctggtaaag catcttaatc agacttattt    1980

ttaattactg aatatttctt agacgttttg ggacagattt tatgtaatct ttataagtat    2040

gatttctgaa gaaaagcaaa tgcattagta tgtttgcctt aaacttgtag actaaaccaa    2100

gtattgtaaa ataaacagcg ataacagtga tagtttttaa ctctatggtc attgtatcac    2160

tctggaaaat gtggagtagc tgtaataaat ctaatcctgt attatgcttt aaaaaaaaaa    2220

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa               2269
```

<210>   26

<211>   1834

<212>   DNA

<213>   Unknown

<220>

<223>   clone S1+27 cDNA sequence

<400>   26
```
gtcgacccac gcgtccggcg ggccgtggga gggtcccgag gtgggggtcg gggcgggatg       60
```

```
gctgcagcgg cggccggggc cgggagcggg ccctgggcgg cccaggagaa gcagttcccg    120

ccggcgctgc tgagtttctt catctacaac ccgcgcttcg ggccgcgcga aggacaggag    180

gaaaataaga tttttatttta tcatccaaat gaggtagaaa agaatgagaa gattagaaat    240

gtcggattgt gtgaagctat tgtacagttt acaaggacat ttagcccatc aaaacctgca    300

aaatctttac atacacagaa gaacagacag ttcttcaatg aaccagaaga aaatttctgg    360

atggtcatgg ttgttcggaa tcctataatt gaaaaacaga gtaaagatgg aaaaccagtt    420

attgaatatc aagaggagga gttgttggac aaggtttata gctcggtgct gcggcagtgc    480

tacagcatgt acaagctttt taatggtaca tttctgaaag ccatggaaga cggaggcgtc    540

aagcttctga aagaaaaatt agagaaattc ttccatcggt atttgcaaac gctacatttg    600

cagtcatgtg acctacttga catttttggt ggaatcagct tcttcccgtt ggataaaatg    660

acttatttga aaatccagtc ctttattaat aagaatggag gaaagcctga atatagtcaa    720

atacactgct tttctctata acgatcagct catctggagt ggattagaac aagatgacat    780

gagaatttta tacaaatacc ttaccacctc ccttttccca aggcacatcg aacctgagtt    840

agcaggaagg gattctccaa taagagcaga aatgccagga aatcttcaac actatggaag    900

atttcttacc ggacccttga acctcaatga tccagatgca aaatgcagat tccccaaaat    960

ttttgtaaat acagatgaca cttatgaaga gctccattta atcgtttata aggccatgag   1020

tgcggctgtg tgctttatga tcgacgcctc tgtccaccca acgttggatt tttgccgaag   1080

actggacagc atcgttgggc cccagctcac agtgctggcc tctgacatct gtgaacagtt   1140

taacatcaac aagaggatgt ccgggtctga gaaagaaccc cagtttaagt ttatctactt   1200

caaccacatg aatctcgccg agaagagcac agttcacatg aggaaaacgc ccagcgtgtc   1260

gctcacttcc gtgcacccgg atttaatgaa gattctcggt gacatcaaca gtgactttac   1320

cagagtggat gaagatgagg agatcattgt gaaggccatg agtgattact gggttgttgg   1380

aaagaagtct gatcggcggg agctctatgt tattttgaat caaaaaaatg caaacctgat   1440

tgaagtaaat gaggtcaaga aactttgtgc aacgcagttc aacaacatct tcttcttgga   1500

ttgacggatg acggctcact gagagcatat ctaaaaaaca ctctgcaaac atttggtcac   1560

atgcaagtta gtggtcatat gacggactgc attcaggaca agggtaaagc aatacttgct   1620

ttgaagaatc acatttcgac tcggtctgct gatctgaggt ttttagattt taaatatta    1680

tgtggaatta attaaaggta gttggctata tcgctatcat ttcattcttt tgacattatg   1740

tgaatatttt actggaaaat aagactaata aattgttaaa agtttttaaa aaaaaaaaa    1800

aaaaaaaaaa aaaaaaaaaa aaaaagggc ggcc                                 1834
```

<210> 27

<211> 2276

<212> DNA

<213> Unknown

<220>

<223> clone S1+28 cDNA sequence

<400> 27

```
gtttgcagtt gatgctaagg ccttgcctca gaataagcca aggcctctca ctcaagaaga      60

aattgctcag agacgtgagc gtgcaagaca aaggcatgca gagaagcttg cagcagcaca     120

gggacaggca cccttggagc ccacccaaga tgggagtgcc attgaaacat gtccaaaagg     180

agacgagcca agaggtgacg agcaacaggt ggaaagtatg acccctaaac ctgtgctcca     240

ggaagaaaac aaccaagagt cttttattgc atttgctcgg gtgttcagtg gtgtggctcg     300

aagaggaaag aaaattttg tcttggggcc caaatacagt cctcttgagt ttttacgaag      360

ggtaccatta tgcttctcag ctccaccaga tggcctcccc caagtccccc acatggcata     420

ctgtgctctg gaaaacctgt atcttctgat gggaagggaa ctggaatatc tagaggaggt     480

acctccagga aatgtgctag gaataggagg ccttcaagat tttgtgctga aatctgcaac     540

actgtgtagc ctgccatcct gcccaccatt tataccactc aacttcgaag ccactcctat     600

tgtgagagtt gctgttgaac caaaacatcc aagtgaaatg cctcagctcg taaaaggaat     660

gaaactgtta aaccaggctg atccctgtgt ccagatttta attcaggaaa cgggagagca     720

cgttttagtc acagcaggag aagtccacct tcagcgatgc ctggatgact aaaagaaag      780

gtttgcaaag attcatatca gtgtatctga acctattatt ccattcagag aaacaatcac     840

aaaacccca aaagttgaca tggtcaatga agaaatagGc aaacagcaaa aagttgcagt      900

catacaccaa atgaaagaag atcaaagcaa aatccctgaa ggaatccaag ttgactctga     960

cgggctaatc accataacaa ctcccaataa acttgccacg ctcagtgttc gagccatgcc    1020

ccttccagaa gaagtcaccc agattctgga agaaaatagt gatttgattc gttctatgga    1080

gcagttgaca tcctctttga atgagggtga aaatactcac atgattcatc agaagaccca    1140

agagaaaatt tgggaattca aaggaaaact ggagcaacac ctaacaggga gaagatggag    1200

gaacattgtt gaccaaatct ggtcatttgg cccaagaaaa tgtgggccca acatactagt    1260

caataaaagt gaagattttc agaactcagt atggacaggt ccagctgaca aagcttcaaa    1320

agaagccagt agataccgag atttgggcaa tagcattgtg agtggcttcc aactagcaac    1380

cctctctggc cccatgtgtg aggagcctct catgggtgtc tgttttgttc tggaaaaatg    1440

ggacctaagt aaatttgagg aacaaggagc aagtgatctg gcaaaagagg acaggaggaa    1500
```

```
aatgaaacct gttctggtgg aaatgaaaac caagagctac aagatggctg ctctgaggcc    1560

tttgagaaga ggacatcaca gaaaggagaa tctccactca ctgactgcta tggacctttc    1620

tcaggacagc taattgccac catgaaagaa gcatgtcgct atgcactgca agtgaaacct    1680

cagcgcctga tggcagctat gtacacatgt gacatcatgg ccactggtga tgttctcggt    1740

cgagtctatg ctgtcttgtc aaagagagaa ggtcgggtac ttcaagaaga aatgaaagaa    1800

gggacagaca tgttcatcat caaggctgtg ctgcctgttg ctgaaagctt tggttttgct    1860

gatgaaatca ggaagaggac aagtggcctg gccagcccac aactagtatt cagccattgg    1920

gagatcattc ccagtgaccc ttctgggtgc caactactga ggaggaatac ttgcactttg    1980

gggagaaggc tgactctgag aaccaagccc ggaagtacat gaacgcagta cgaaagcgga    2040

aggggcttta tgtggaagaa aagattgtgg agcatgcaga aaagcagagg acactcagca    2100

aaaataagta gctacctact actggtggat tcttttcctt atagtgaatt taaaagtatc    2160

atcaagggtt taatattggg aaaatttctt tttgccacat tatctctgtt tattcacttt    2220

caataaagtt gatccatata aatattttaa agaggatgtt aaaaaaaaaa aaaaaa       2276
```

<210> 28

<211> 8

<212> PRT

<213> Unknown

<220>

<223> Starting sequence of SIP2

<400> 28

Met Glu Glu Ser Leu Asn Ile Val
1   5